- An oligonucleotide (oligo #1, SEQ ID NO: 1) comprising nucleotides 374-403 of the E6 gene of human papilloma virus type 16 was synthesized by the phosphoramidite method of DNA synthesis and labeled with ^{32}P at the 5′ end. A second ^{32}P-labeled oligonucleotide (oligo #2, SEQ ID NO: 2) containing the same sequence as oligo #1 (SEQ ID NO: 1) except for a single G->A base change at position 388 was also prepared.

Oligo #1, SEQ ID NO: 1: 5′-CAA TAC AAC AAA CCG TTG TGT GAT TTG TTA-3′

Oligo #2, SEQ ID NO: 2: 5′-CAA TAC AAC AAA CCA TTG TGT GAT TTG TTA-3′-

Please replace the paragraph starting on page 9, line 32, with the following rewritten paragraph:

-A 20-mer DNA probe (oligo #3, SEQ ID NO: 3) containing the photoactive cross-linking group, 3-*O*-(7-coumarinyl) glycerol (denoted by N in the sequence) was prepared. This DNA sequence of this probe is fully complementary to oligo #1 (SEQ ID NO: 1) but would hybridize with oligo #2 (SEQ ID NO: 2) to form a duplex containing an A/C mismatch.

Oligo #3, SEQ ID NO: 3: 3′-TTG TTT GGC AAC ACA CTA NA-5′

Oligo #1/#3 duplex:

SEQ ID NO: 1 5′-CAA TAC AAC AAA CCG TTG TGT GAT TTG TTA-3′
SEQ ID NO: 3 3′-TTG TTT GGC AAC ACA CTA NA-5′

Oligo #2/#3 duplex:

SEQ ID NO: 2 5′-CAA TAC AAC AAA CCA TTG TGT GAT TTG TTA-3′
SEQ ID NO: 3 3′-TTG TTT GGC AAC ACA CTA NA-5′ -

Please replace the paragraph starting on page 10, line 10, with the following rewritten paragraph:

-Oligo #3, SEQ ID NO: 3 (20 pmole) was incubated in the presence of 2 pmole of either ^{32}P-5' end-labeled oligo #1 (SEQ ID NO: 1) or oligo #2 (SEQ ID NO: 2) in 0.15 mL samples at the temperatures and NaCl concentrations summarized below:-

Please replace the paragraph starting on page 11, line 1, with the following rewritten paragraph:

--By carrying out the experiment under a range of hybridization temperatures (45-55°C) and NaCl concentration (150-300 mM), it was possible to define conditions that led to appreciable cross-link formation between the complementary oligonucleotides #1 (SEQ ID NO: 1) and #3 (SEQ ID NO: 3) but not the mismatched oligonucleotides #2 (SEQ ID NO: 2) and #3(SEQ ID NO: 3). To determine the best conditions for mismatch discrimination the radioactive bands were excised from the gel, quantified by scintillation counting and the percent yield of cross-linked product measured (relative to unreacted ^{32}P-labeled oligonucleotide). The results are shown below:--

Please replace the paragraph starting on page 11, line 32, with the following rewritten paragraph:

-Analysis of the autoradiogram for the samples (3 and 4) run under the least stringent hybridization conditions (45°C, 300 mM NaCl) clearly showed that the product obtained from cross-linking between the mismatched oligonucleotides #2 (SEQ ID NO: 2) and #3 (SEQ ID NO: 3) migrated slower through the gel than the product obtained from cross-linking the complementary oligonucleotides #1 (SEQ ID NO: 1) and #3 (SEQ ID NO: 3) (the DSCP effect).--

Please replace the paragraph starting on page 12, line 7, with the following rewritten paragraph:

--2. By using non-stringent conditions the cross-link yield and hence the signal in the assay is higher than when the hybridization stringency method is employed; under the conditions used for DSCP analysis (45°C, 300 mM NaCl) the cross-link yield for the reaction between the complementary oligonucleotides #1 (SEQ ID NO: 1) and #3 (SEQ ID NO: 3) was 49%, however under the conditions that led to the best mismatch discrimination with the hybridization stringency method (55°C, 150 mM NaCl), the cross-linking efficiency was 39%. Thus the DSCP method resulted in 26% greater signal.--

Please replace the paragraph starting on page 12, line 18, with the following rewritten paragraph:

--Two 56 base oligonucleotides comprising a portion of the sequence of either the normal human β-globin gene (β^A-target) or the sickle cell β-globin

gene (β^S-target) were synthesized by the phosphoramidite method of DNA synthesis and labeled with ^{32}P at their 5' ends. The β^S-globin target sequence differs from the β^A-target by a single A->T mutation that gives raise to a mutant β-globin protein that contains valine instead of glutamic acid.

β^A-target: 5'-TGA CTC CTG AGG AGA AGT CTG CCG TTA CTG CCC TGT-
GGG GCA AGG TGA ACG TGG AT-3' (SEQ ID NO: 4)

β^S-target: 5'-TGA CTC CTG TGG AGA AGT CTG CCG TTA CTG CCC TGT-
GGG GCA AGG TGA ACG TGG AT-3' (SEQ ID NO: 5)--

Please replace the paragraph starting on page 12, line 28, with the following rewritten paragraph:

--Two probes complementary to either the β^A-target sequence (β^A-probe) or the β^S-target (β^S-probe) were also synthesized. These probes were modified with the photoactive cross-linking group, 3-O-(7-coumarinyl) glycerol (denoted by N in the sequence):

β^A-probe: 3'-TGA GGA CTC CTC TTC ANA-5' (SEQ ID NO: 6)

β^S-probe: 3'-TGA GGA CAC CTC TTC ANA-5' (SEQ ID NO: 7)--

On page 15, immediately preceding the claims, insert the enclosed text entitled "SEQUENCE LISTING".

REMARKS

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "Version with markings to show changes made."

These amendments are made in adherence with 37 C.F.R. § 1.821-1.825. This amendment is accompanied by a floppy disc containing the above named sequence, SEQUENCE ID NUMBERS 1-7, in computer readable form, and a paper copy of the sequence information. The computer readable sequence listing was prepared through use of the software program "Patent-In" provided by the PTO. The information contained in the computer readable disk is identical to that of the paper copy. This amendment contains no new matter. Applicant submits that this amendment, the accompanying